

## Reviewer Report

**Title:** Draft genome assembly of the Bengalese finch, *Lonchura striata domestica*, a model for motor skill variability and learning

**Version:** Original Submission    **Date:** 26 Nov 2017

**Reviewer name:** Niclas Backström

### Reviewer Comments to Author:

Comments to manuscript GIGA-D-17-00224.

#### General:

The manuscript by Colquitt et al. is a short technical note presenting the development of a draft genome assembly and a set of RNAseq data sets for the Bengalese finch. Besides the assembly stats comparison to previously published avian genomes in the frame-work of the avian genomics consortium, the manuscript contains no analyses. Hence, this review only considers the rationale behind selecting this particular species and the technical aspects of generating the data. The manuscript is well written and easy to follow.

The authors state that the Bangalese finch could develop into a model system for understanding the genetic basis of vocal learning, in particular of song variability and plasticity. In the introduction, the authors make a thorough review of the status of the Bengalese finch in the field of vocal learning. Admittedly, I was initially a bit surprised that the manuscript contained such a detailed introduction describing the study organism but after several rounds of reading I conclude that this strengthens the paper and makes the rationale behind developing genomic tools for this species well supported.

The methods section clearly states how the data was collected and edited before submission to data bases. I could access the data via the links provided so it should be accessible for researchers interested in using these data for analyses. The data was curated with standard methods in the field. My only concerns regard, i) the manual curation of the gene models which could be described in more detail (did you omit ORF:s out of frame?, change the sequence to get ORF in frame?, how was UTR positions determined?, etc.), and, ii) a better description of the rationale behind selecting the particular tissues/sexes for RNAseq.

#### Detailed comments:

L71 omit 'the'

L83 Is this statement correct? Several songbirds have very high-quality assemblies available (eg. *Ficedula albicollis*, *Corvus corone*).

L100 It is stated that the Bengalese finch has high level of genetic polymorphism - in the range of

outbred human populations. Most songbirds have considerably higher polymorphism levels than that. I would suggest to present this in a different way and give the estimated theta values.

L130 Maybe provide approved animal use protocol (ID number).

L182 Ref for TrimGalore!

L190-191. Please, provide dates for accession/download since these data bases sometimes change.

L202-203. As far as I am aware CEGMA is not recommended anymore after the BUSCO tool was developed. The CEGMA part can hence be omitted. Unclear here also how 65% can be complete and 94% partial CEGs?

L332 typos; of, shown?

### **Level of Interest**

Please indicate how interesting you found the manuscript: An article of limited interest

### **Quality of Written English**

Please indicate the quality of language in the manuscript: Acceptable

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